

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/643, 801A  
Source: 1000 - EFS  
Date Processed by STIC: 6-28-05

***ENTERED***



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/643,801A

DATE: 06/28/2005

TIME: 15:14:22

Input Set : N:\efs\10643801A\_efs\RTS0678USSEQ.txt  
 Output Set: N:\CRF4\06282005\J643801A.raw

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3 <110> APPLICANT: Sanjay Bhanot
4      Kenneth W. Dobie
6 <120> TITLE OF INVENTION: MODULATION OF DIACYLGLYCEROL ACYLTRANSFERASE 2 EXPRESSION
8 <130> FILE REFERENCE: RTS-0678US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/643,801A
C--> 10 <141> CURRENT FILING DATE: 2003-08-18
10 <160> NUMBER OF SEQ ID NOS: 233
13 <210> SEQ ID NO: 1
14 <211> LENGTH: 20
15 <212> TYPE: DNA
16 <213> ORGANISM: Artificial Sequence
18 <220> FEATURE:
20 <223> OTHER INFORMATION: Antisense Oligonucleotide
22 <400> SEQUENCE: 1
23 tccgtcatcg ctcctcaggg                                20
26 <210> SEQ ID NO: 2
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
33 <223> OTHER INFORMATION: Antisense Oligonucleotide
35 <400> SEQUENCE: 2
36 gtgcgcgcga gcccgaatc                                20
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 20
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
46 <223> OTHER INFORMATION: Antisense Oligonucleotide
48 <400> SEQUENCE: 3
49 atgcattctg ccccaagga                                20
52 <210> SEQ ID NO: 4
53 <211> LENGTH: 2439
54 <212> TYPE: DNA
55 <213> ORGANISM: H. sapiens
57 <220> FEATURE:
59 <220> FEATURE:
60 <221> NAME/KEY: CDS
61 <222> LOCATION: (231)...(1397)
63 <400> SEQUENCE: 4
64 ctccggaaac gccagcgcgcg cggtgcgcgc ctctgtggg gtctaggctg tttctctcg 60
66 gccaccactg gcccggggcc gcagctccag gtgtcttagc cggccagcct cgacgccgtc 120
68 ccgggacccc tgtgctctgc gcaagccct ggccccgggg gcccgggcat gggccagggg 180

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70	cgccgggtga	agcggcttcc	cgcggggccg	tgactggcgcg	ggcttcagcc	atg aag	236
71						Met Lys	
72						1	
74	acc ctc ata	gcc gcc tac	tcc ggg gtc	ctg cgc ggc	gag cgt cag	cgc	284
75	Thr Leu Ile Ala	Ala Tyr Ser Gly	Val Leu Arg Gly	Glu Arg Gln	Ala		
76	5	10	15				
78	gag gct gac	cgg agc cag	cgc tct cac	gga gga cct	gcg ctg tcg	cgc	332
79	Glu Ala Asp	Arg Ser Gln Arg	Ser His Gly	Gly Pro Ala	Leu Ser	Arg	
80	20	25	30				
82	gag ggg tct	ggg aga tgg	ggc act gga	tcc agc atc	ctc tcc gcc	ctc	380
83	Glu Gly Ser	Gly Arg Trp	Gly Thr Gly	Ser Ser Ile	Leu Ser Ala	Leu	
84	35	40	45			50	
86	cag gac ctc	ttc tct gtc	acc tgg ctc	aat agg tcc	aag gtg gaa	aag	428
87	Gln Asp Leu Phe	Ser Val Thr Trp	Leu Asn Arg	Ser Lys Val	Glu Lys		
88	55	60	65				
90	cag cta cag	gtc atc tca	gtg ctc cag	tgg gtc ctg	tcc ttc ctt	gta	476
91	Gln Leu Gln Val	Ile Ser Val	Leu Gln Trp	Val Leu Ser	Phe Leu	Val	
92	70	75	80				
94	ctg gga gtg	gcc tgc agt	gcc atc ctc	atg tac ata	tcc tgc act	gat	524
95	Leu Gly Val	Ala Cys Ser	Ala Ile Leu	Met Tyr Ile	Phe Cys Thr	Asp	
96	85	90	95				
98	tgc tgg ctc	atc gct gtg	ctc tac ttc	act tgg ctg	gtg ttt gac	tgg	572
99	Cys Trp Leu Ile	Ala Val Leu	Tyr Phe Thr	Trp Leu Val	Phe Asp	Trp	
100	100	105	110				
102	aac aca ccc	aag aaa ggt	ggc agg agg	tca cag tgg	gtc cga aac	tgg	620
103	Asn Thr Pro	Lys Lys Gly	Gly Arg Arg	Ser Gln Trp	Val Arg Asn	Trp	
104	115	120	125			130	
106	gct gtg tgg	cgc tac ttt	cga gac tac	ttt ccc atc	cag ctg gtg	aag	668
107	Ala Val Trp Arg	Tyr Phe Arg Asp	Tyr Phe Pro	Ile Gln Leu	Val Lys		
108	135	140	145				
110	aca cac aac	ctg ctg acc	acc agg aac	tat atc ttt	gga tac cac	ccc	716
111	Thr His Asn	Leu Leu Thr	Thr Arg Asn	Tyr Ile Phe	Gly Tyr His	Pro	
112	150	155	160				
114	cat ggt atc	atg ggc ctg	ggt gcc ttc	tgc aac ttc	agc aca gag	gcc	764
115	His Gly Ile	Met Gly Leu	Gly Ala Phe	Cys Asn Phe	Ser Thr Glu	Ala	
116	165	170	175				
118	aca gaa gtg	agc aag aag	ttc cca ggc	ata cgg cct	tac ctg gct	aca	812
119	Thr Glu Val	Ser Lys Lys	Phe Pro Gly	Ile Arg Pro	Tyr Leu Ala	Thr	
120	180	185	190				
122	ctg gca ggc	aac ttc cga	atg cct gtg	ttg agg gag	tac ctg atg	tct	860
123	Leu Ala Gly	Asn Phe Arg	Met Met Pro	Val Leu Arg	Glu Tyr Leu	Met Ser	
124	195	200	205			210	
126	gga ggt atc	tgc cct gtc	agc cgg gac	acc ata gac	tat ttg ctt	tca	908
127	Gly Gly Ile	Cys Pro Val	Ser Arg Asp	Thr Ile Asp	Tyr Leu	Leu Ser	
128	215	220	225				
130	aag aat ggg	agt ggc aat	gct atc atc	gtg gtc	ggg ggt gcg	gct	956
131	Lys Asn Gly	Ser Gly Asn	Ala Ile Ile	Ile Val Val	Gly Ala	Ala	
132	230	235	240				
134	gag tct ctg	agc tcc atg	cct ggc aag	aat gca gtc	acc ctg	cg aac	1004

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135	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	Leu	Arg	Asn	
136			245				250						255				
138	cgc	aag	ggc	ttt	gtg	aaa	ctg	gcc	ctg	cgt	cat	gga	gct	gac	ctg	gtt	1052
139	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	Ala	Asp	Leu	Val	
140							260			265			270				
142	ccc	atc	tac	tcc	ttt	gga	gag	aat	gaa	gtg	tac	aag	cag	gtg	atc	ttc	1100
143	Pro	Ile	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	Lys	Gln	Val	Ile	Phe	
144	275				280						285			290			
146	gag	gag	ggc	tcc	tgg	ggc	cga	tgg	gtc	cag	aag	ttc	cag	aaa	tac		1148
147	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Gln	Lys	Lys	Phe	Gln	Lys	Tyr	
148					295					300			305				
150	att	ggt	ttc	gcc	cca	tgc	atc	ttc	cat	gtt	cga	ggc	ctc	ttc	tcc	tcc	1196
151	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	Gly	Arg	Gly	Leu	Phe	Ser	Ser	
152				310					315			320					
154	gac	acc	tgg	ggg	ctg	gtg	ccc	tac	tcc	aag	ccc	atc	acc	act	gtt	gtg	1244
155	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	Ser	Lys	Pro	Ile	Thr	Thr	Val	Val	
156			325				330				335.						
158	gga	gag	ccc	atc	acc	atc	ccc	aag	ctg	gag	cac	cca	acc	cag	caa	gac	1292
159	Gly	Glu	Pro	Ile	Thr	Ile	Pro	Lys	Leu	Glu	His	Pro	Thr	Gln	Gln	Asp	
160			340				345				350						
162	atc	gac	ctg	tac	cac	acc	atg	tac	atg	gag	gcc	ctg	gtg	aag	ctc	ttc	1340
163	Ile	Asp	Leu	Tyr	His	Thr	Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu	Phe	
164	355				360					365			370				
166	gac	aag	cac	aag	aag	ttc	ggc	ctc	ccg	gag	act	gag	gtc	ctg	gag		1388
167	Asp	Lys	His	Lys	Thr	Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu	Glu	
168					375				380			385					
170	gtg	aac	tga	gccagccttc	ggggccaact	ccctggagga	accagctgca	aatcactttt									1447
171	Val	Asn															
173	ttgctctgta	aatttggaaag	tgtcatgggt	gtctgtgggt	tatttaaaag	aaattataac											1507
175	aattttgcta	aaccattaca	atgttaggtc	ttttttaaga	aggaaaaagt	cagtatttca											1567
177	agttcttca	cttccagctt	gccctgttct	agggttgtgg	taaatctggg	cctaattctgg											1627
179	gtggctcagc	taacctctct	tcttcccttc	ctgaagtgac	aaaggaaact	cagtcttctt											1687
181	ggggagaagaag	gattgccatt	agtgaatttg	accagttaga	tgattcactt	tttgcccccta											1747
183	gggatgagag	gcgaaagcca	cttctcatac	aagccccctt	attgccacta	ccccacgctc											1807
185	gtctagtcct	gaaactgcag	gaccagtttc	tctgccaagg	ggaggagttt	gagagcacag											1867
187	ttgccccgtt	gtgtgagggc	agtagtaggc	atctggatg	ctccagttt	atctcccttc											1927
189	tgccacccct	acctcacc	cc	tagtactca	tatcgagcc	tggactggcc	tccaggatga										1987
191	ggatgggggt	ggcaatgaca	ccctgcaggg	gaaaggactg	ccccccatgc	accattgcag											2047
193	ggaggatgcc	gccaccatga	gctaggtgga	gtaactgggt	tttcttggtt	ggctgatgac											2107
195	atggatgcag	cacagactca	gccttggcct	ggagcacatg	cttactgggt	gcctcagttt											2167
197	accttcccca	gatccttagat	tctggatgt	aggaagagat	cccttcttcag	aaggggcctg											2227
199	gccttctgag	cagcagatta	gttccaaagc	aggtggcccc	cgaacccaag	cctcactttt											2287
201	ctgtgccttc	ctgagggggt	tgggcccggg	aggaaaccca	accctctcct	gtgtgttctg											2347
203	ttatctcttg	atgagatcat	tgcaccatgt	cagactttt	tatatgcctt	gaaaataaaat											2407
205	gaaaatgaga	atccaaaaaa	aaaaaaaaaa	aa													2439
208	<210>	SEQ ID NO:	5														
209	<211>	LENGTH:	22														
210	<212>	TYPE:	DNA														
211	<213>	ORGANISM:	Artificial Sequence														

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213 <220> FEATURE:
215 <223> OTHER INFORMATION: PCR Primer
217 <400> SEQUENCE: 5
218 catacggcct tacctggcta ca 22
221 <210> SEQ ID NO: 6
222 <211> LENGTH: 24
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
228 <223> OTHER INFORMATION: PCR Primer
230 <400> SEQUENCE: 6
231 cagacatca gta tccccc aaca 24
234 <210> SEQ ID NO: 7
235 <211> LENGTH: 22
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
241 <223> OTHER INFORMATION: PCR Probe
243 <400> SEQUENCE: 7
244 tggcaggcaa ctccgaatg cc 22
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 19
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
254 <223> OTHER INFORMATION: PCR Primer
256 <400> SEQUENCE: 8
257 gaagggtgaag gtccggagtc 19
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 20
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
267 <223> OTHER INFORMATION: PCR Primer
269 <400> SEQUENCE: 9
270 gaagatgggt atgggatttc 20
273 <210> SEQ ID NO: 10
274 <211> LENGTH: 20
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
280 <223> OTHER INFORMATION: PCR Probe
282 <400> SEQUENCE: 10
283 caagcttccc gttctcagcc 20
286 <210> SEQ ID NO: 11
287 <211> LENGTH: 2262
288 <212> TYPE: DNA
289 <213> ORGANISM: M. musculus
291 <220> FEATURE:

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293 <220> FEATURE:
294 <221> NAME/KEY: CDS
295 <222> LOCATION: (207)...(1373)
297 <400> SEQUENCE: 11
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300 ttcgcgcctg ctgcgcgcac ggcctggcg ctgtccctca gctcccgag ctcagcgcga      120
302 agccctggcc ccggccggccg gggcatgggt caggggcgcg gcgtgagcgc gctttctgca      180
304 cggccgtgac gtgcattggc ttcagc atg aag acc ctc atc gcc gcc tac tcc      233
305                               Met Lys Thr Leu Ile Ala Ala Tyr Ser
306                               1           5
308 ggg gtc ctg cgg ggt gag cgt cgg gcg gaa gct gcc cgc agc gaa aac      281
309 Gly Val Leu Arg Gly Glu Arg Arg Ala Glu Ala Ala Arg Ser Glu Asn
310   10          15          20          25
312 aag aat aaa gga tct gcc ctg tca cgc gag ggg tct ggg cga tgg ggc      329
313 Lys Asn Lys Gly Ser Ala Leu Ser Arg Glu Gly Ser Gly Arg Trp Gly
314          30          35          40
316 act ggc tcc agc atc ctc tca gcc ctc caa gac atc ttc tct gtc acc      377
317 Thr Gly Ser Ser Ile Leu Ser Ala Leu Gln Asp Ile Phe Ser Val Thr
318          45          50          55
320 tgg ctc aac aga tct aag gtg gaa aaa cag ctg cag gtc atc tca gta      425
321 Trp Leu Asn Arg Ser Lys Val Glu Lys Gln Leu Gln Val Ile Ser Val
322          60          65          70
324 cta caa tgg gtc cta tcc ttc ctg gtg cta gga gtg gcc tgc agt gtc      473
325 Leu Gln Trp Val Leu Ser Phe Leu Val Leu Gly Val Ala Cys Ser Val
326          75          80          85
328 atc ctc atg tac acc ttc tgc aca gac tgc tgg ctg ata gct gtg ctc      521
329 Ile Leu Met Tyr Thr Phe Cys Thr Asp Cys Trp Leu Ile Ala Val Leu
330          90          95          100          105
332 tac ttc acc tgg ctg gca ttt gac tgg aac acg ccc aag aaa ggt ggc      569
333 Tyr Phe Thr Trp Leu Ala Phe Asp Trp Asn Thr Pro Lys Lys Gly Gly
334          110         115          120
336 agg aga tcg cag tgg gtg cga aac tgg gcc gtg tgg cgc tac ttc cga      617
337 Arg Arg Ser Gln Trp Val Arg Asn Trp Ala Val Trp Arg Tyr Phe Arg
338          125         130          135
340 gac tac ttt ccc atc cag ctg gtg aag aca cac aac ctg ctg acc acc      665
341 Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr His Asn Leu Leu Thr Thr
342          140         145          150
344 agg aac tat atc ttt gga tac cac ccc cat ggc atc atg ggc ctg ggt      713
345 Arg Asn Tyr Ile Phe Gly Tyr His Pro His Gly Ile Met Gly Leu Gly
346          155         160          165
348 gcc ttc tgt aac ttc agc aca gag gct act gaa gtc agc aag aag ttt      761
349 Ala Phe Cys Asn Phe Ser Thr Glu Ala Thr Glu Val Ser Lys Lys Phe
350          170         175          180          185
352 cct ggc ata agg ccc tat ttg gct acg ttg gct ggt aac ttc cgg atg      809
353 Pro Gly Ile Arg Pro Tyr Leu Ala Thr Leu Ala Gly Asn Phe Arg Met
354          190         195          200
356 cct gtg ctt cgc gag tac ctg atg tct gga ggc atc tgc cct gtc aac      857
357 Pro Val Leu Arg Glu Tyr Leu Met Ser Gly Gly Ile Cys Pro Val Asn
358          205         210          215

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No  
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1241 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:  
L:3831 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:3835 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:232  
L:3846 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!  
L:3850 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:233